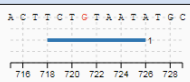
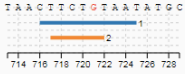
Supplementary Figure S1

A

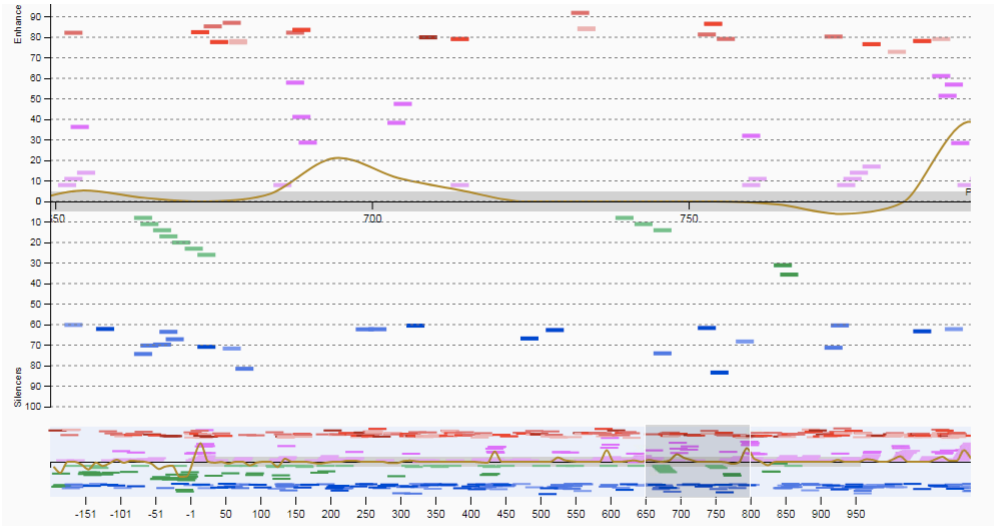
Interpreted Data

This table shows only relevant results related to the mutation position and context.
The mutation occurs in the late exonic positions, the following table show results of donor splice sites, ESE and ESS that could be affected by the mutation

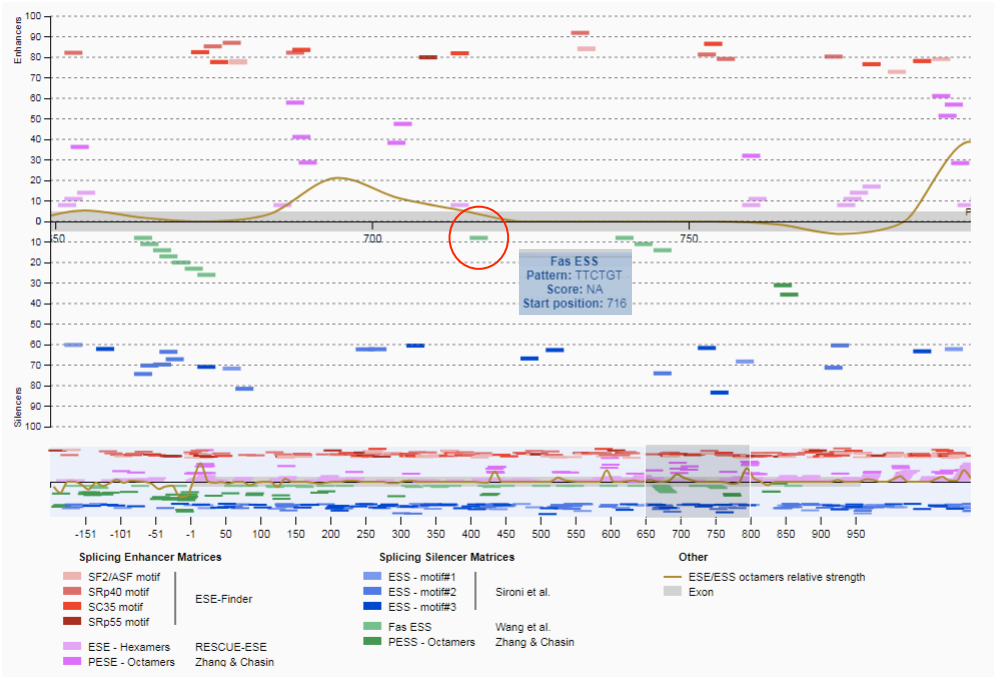
Predicted signal	Prediction algorithm	cDNA Position	Interpretation
New Donor Site	1 - HSF Matrices		Activation of an exonic cryptic donor site. Potential alteration of splicing.
New ESS Site	1 - IIEs from Zhang et al.		Creation of an exonic ESS site. Potential alteration of splicing.
	2 - Fas-ESS hexamers		

B

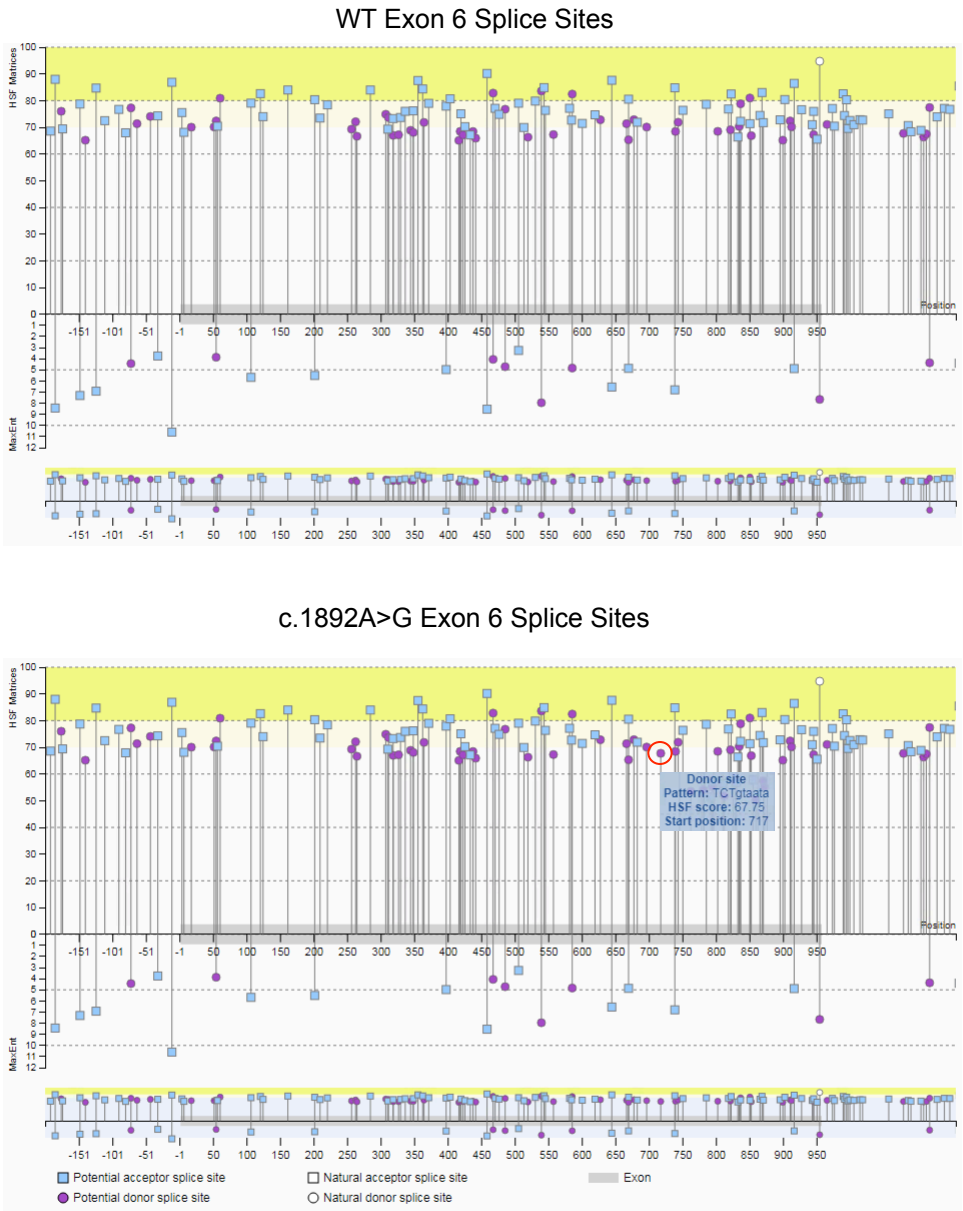
WT Exon 6 Splice Motifs



c.1892A>G Exon 6 Splice Motifs

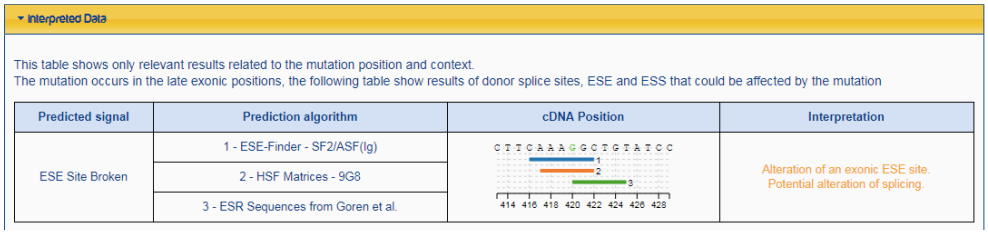


C

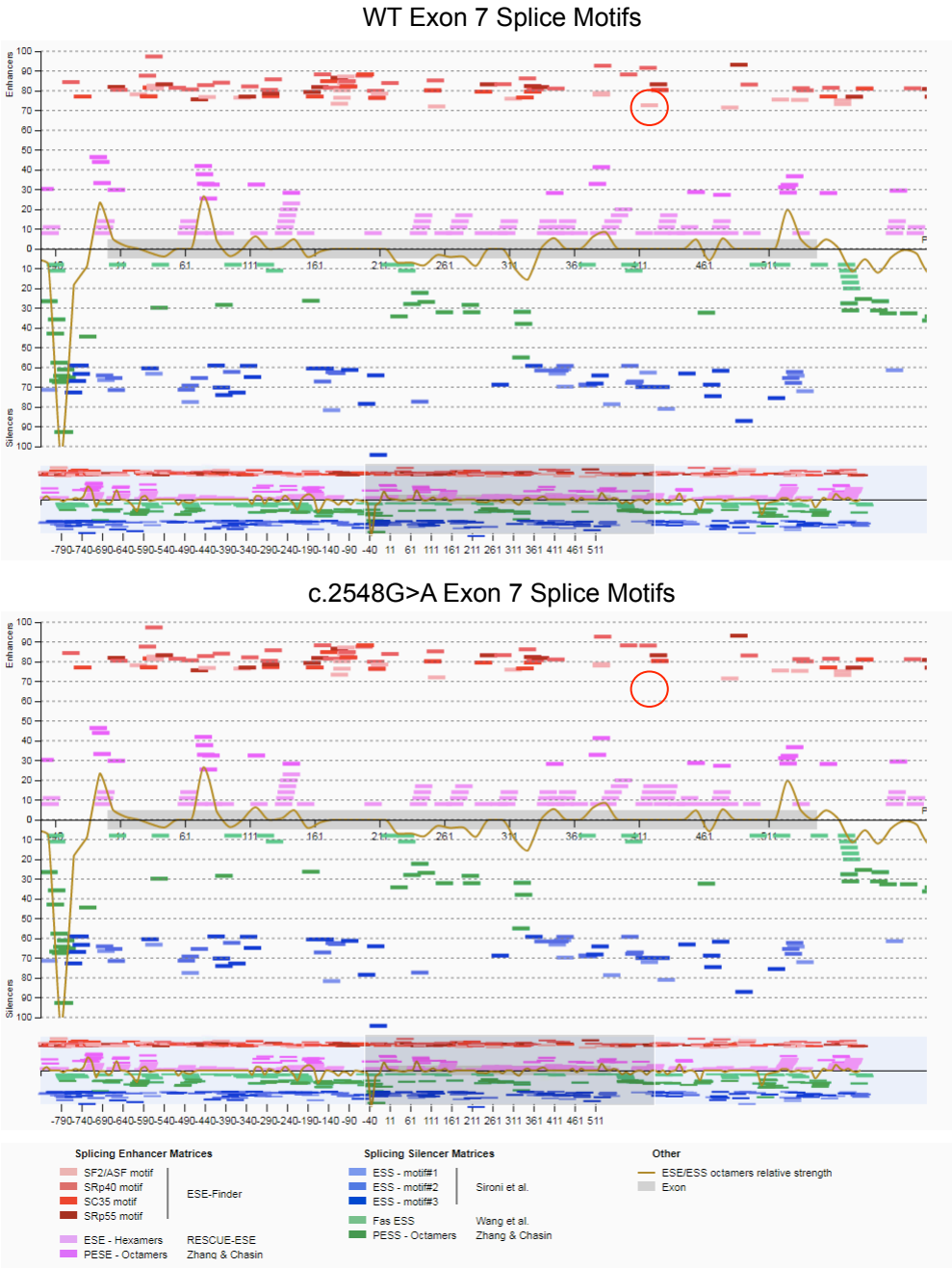


Supplementary Figure S1. Human Splicing Finder Analysis of the c.1892A>G variant. A 2kb sequence incorporating *CRB1* exon 6 and surrounding intronic sequences was selected for analysis of local splicing motifs using Human Splicing Finder version 3.1. **(A)** We first used the *Analyze a mutation* function to compare the c.1892A>G variant with the normal sequence. The Interpreted Results output panel indicated potential alterations of splicing due to the activation of a cryptic splice site and the creation of an exonic splice silencer (ESS). **(B-C)** We used the *Analyze a sequence* function to identify splice motifs (**B**) and splice sites (**C**) in the c.1892A>G variant and the normal sequence. The location of the ESS and cryptic splice site generated are indicated by the red circles.

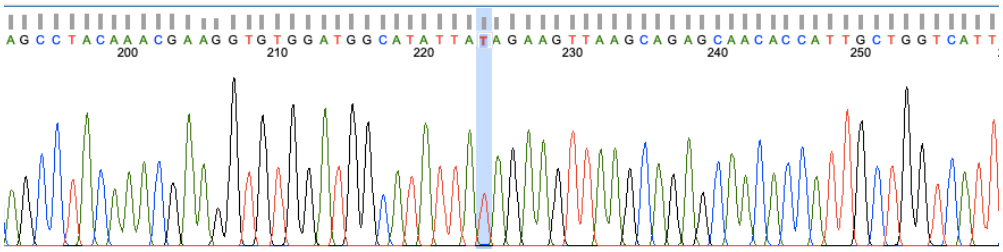
a



b



Supplementary Figure S2. Human Splicing Finder Analysis of the c.2548G>A variant. A 2kb sequence incorporating *CRB1* exon 7 and surrounding intronic sequences was selected for analysis of local splicing motifs using Human Splicing Finder version 3.1. **(A)** We first used the *Analyze a mutation* function to compare the c. 2548G>A variant with the normal sequence. The Interpreted Results output panel indicated potential alterations of splicing due to the alteration of an exonic splice enhancer (ESE). **(B)** We used the *Analyze a sequence* function to identify splice motifs in the c.2548G>A variant and the normal *CRB1* sequence. The location of a high scoring ESE lost due to the c.2548G>A mutation is indicated by the red circles. Other changes to the local ESE and ESS landscape were also predicted, including the generation of several low scoring ESEs (pink lines) as well as a new ESS (blue lines).



Supplementary Figure S3. PCR screening was performed using primers targeting *CRB1* exons 6 and 7. A 0.5kb PCR band was amplified from proband NRO cDNA then purified and sequenced using the reverse primer. A single 'T' peak was detected at position c.1892 (blue highlight), indicating the detected transcript was derived from the c.2548G>A allele.